

## SEQUENCE LISTINGS

<110> INJE UNIVERSITY

<120> CANCER CELL TARGETING GENE DELIVERY METHOD

<130> PCA31275/IJU

<160> 11

<170> KopatentIn 1.71

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Env F primer

<400> 1

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36

<210> 2

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> 597LN primer

<400> 2

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47

<210> 3

<211> 49

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; LC597 primer

&lt;400&gt; 3

caaccccgcc gcaggtggag gaggcagtga atggactcaa aaatttcaa

49

&lt;210&gt;

4

&lt;211&gt;

35

&lt;212&gt;

DNA

&lt;213&gt;

Artificial Sequence

&lt;220&gt;

&lt;223&gt; Spike R2 primer

&lt;400&gt; 4

tgctctagaa ttcttaaagg ttaccttcgt tctct

35

&lt;210&gt;

5

&lt;211&gt;

36

&lt;212&gt;

DNA

&lt;213&gt;

Artificial Sequence

&lt;220&gt;

&lt;223&gt; LnkNScFv primer

&lt;400&gt; 5

ggaggtggtg gcagccaggt ccagctagtg cagtct

36

&lt;210&gt;

6

&lt;211&gt;

36

&lt;212&gt;

DNA

&lt;213&gt;

Artificial Sequence

&lt;220&gt;

&lt;223&gt; ScFvLnkC primer

&lt;400&gt;

6

actgcctcct ccacctgcgg cgggggttgaa gtccca

36

<210> 7  
 <211> 2058  
 <212> DNA  
 <213> SEAT0 type of GaLV Env glycoprotein

<220>  
 <221> sig\_peptide  
 <222> (1)..(126)

<220>  
 <221> misc\_feature  
 <222> (127)..(1467)  
 <223> surface subunit region

<220>  
 <221> misc\_feature  
 <222> (1468)..(2025)  
 <223> transmembrain domain

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 atgagtcctg ggagctggaa aagactgata atcctcttaa gctgcgtatt cggcggcggc 120  
 gggacgagtc tgcaaaataa gaacccccac cagcccatga cctcacttg gcaggctactg 180  
 tcccaaactg gagacgttgt ctgggataca aaggcagtc agcccccttg gacttggtgg 240  
 cccacactta aacctgatgt atgtgccttg gcggtagtc ttgagtcctg ggatatcccg 300  
 ggaaccgatg tctcgtctc taaacgagtc agacctcgg actcagacta tactgccgct 360  
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 tgcggggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt 540  
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ggccccctt attatgaagc aatagcctca tcaggagagg tcgcctactc caccgacctt	1140
gaccggtgcc gctggggggac ccaaggaaaag ctcacctca ctgaggtctc aggacacggg	1200
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caagactcag tcagcaagtt agaggactca ctgacttccc tgcgcgaggt agtgcctcaa	1680
aataggagag gccttgactt gctgtttcta aaagaagggt gcctctgtgc ggcctaaag	1740
gaagagtgtc gtttttcat agaccactca ggtgcagtac gggactccat gaaaaactc	1800
aaagaaaaac tggataaaag acagttagag cgccagaaaa gccaaaactg gtatgaagga	1860
tggttcaata actccccttg gttaactacc ctgctatcaa ccatcgctgg gccctatta	1920

ctctctcttc tgttgctcat cctcggggcca tgcatcatca ataagttagt tcaattcatc 1980  
 aatgatagga taagtgcagt taaaattctg gtccttagac aaaaatatca ggccctagag 2040  
 aacgaaggta acctttaa 2058

<210> 8  
 <211> 786  
 <212> DNA  
 <213> Tag-72pS1

<220>  
 <221> misc\_feature  
 <222> (346)..(390)  
 <223> (Gly4Ser)3 linker

<220>  
 <221> misc\_feature  
 <222> (739)..(777)  
 <223> PreS1 Tag

<400> 8  
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 tcttgcaggc cttctggcta cacccttact gaccatgcaa ttactgggt gcgccaggcc 120  
 cctggacaac gccttgagtg gatgggatat tttctcctg gcaacgatga ttttaaatac 180  
 tcccagaagt tccagggacg cgtgacaatc actgcagaca aatccgagag cacagcctac 240  
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 aacatggcat actggggcca agggactctg gtcactgtct cttcagggtg aggcggttca 360  
 ggccgagggtg gctctggcgg tggcggatcg gacattgtga tgaccagtc tccagactcc 420  
 ctggctgtgt ctctgggcga gagggccacc atcaactgca agtccagcca gagtgtttta 480  
 tacagcagca acaataagaa ctacttagct tggtagcagc agaaaccagg acagcctcct 540

aagctgctca tttactgggc atctaccogg gaatccgggg tccctgaccg attcagtggc 600  
 agcgggtctg ggacagattt cactctcacc atcagcagcc tgcaggctga agatgtggca 660  
 gtttattact gtcagcaata ttattcctat ccgttgacgt tcggccaagg gaccaagggt 720  
 gaaatcaaag cggccgcagg agccaacgca aacaatccag attgggactt caaccccgcc 780  
 gcatag 786

<210> 9  
 <211> 13  
 <212> PRT  
 <213> PreS1 epitope at C-terminal of Tag-72pS1

<400> 9  
 Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro  
 1 5 10

<210> 10  
 <211> 2871  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> ScFv-GaLV Env GP chimeric peptide (FvGEL199) DNA

<400> 10  
 atggtattgc tgcctgggtc catgttctc acctcaaacc tgcaccacct tcggcaccag 60  
 atgagtcctg ggagctggaa aagactgata atctcttaa gctgcgtatt cggcggcggc 120  
 gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtactg 180  
 tccaaactg gagacgttgt ctgggataca aaggcagtc agcccccttg gacttggtgg 240  
 ccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggataatccg 300  
 ggaaccgatg tctcgtctc taaacgagtc agacctccg actcagacta tactgccgct 360  
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gcaagctcta ccttctacgt atgtccccgg gatggccgga ccctttcaga agctagaagg	480
tgcggggggc tagaaiccci aiacigiaaa gaaigggaii gigagaccac ggggaccggi	540
tattggctat ctaaatcctc aaaagacctc ataactgtaa aatgggacca aaatagcgga	600
ggtggtggca gccagggtcca gctagtgcag tctggggctg aagtgaagaa gcctggggct	660
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cagaccggct ggtgtaaccc ccttaaaata gatttcacag acaaaggaaa attatccaag	1500
gactggataa cgggaaaaac ctggggatta agattctatg tgtctggaca tccaggcgta	1560
cagttcacca ttgccttaaa aatcaccaac atgccagctg tggcagtagg tcctgacctc	1620
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gccactgagt ctgtctggct ttgtttggcc atggggcccc cttattatga agcaatagcc	1920
tcatcaggag aggtgccta ctccaccgac ctgaccggt gccgctggg gaccaagga	1980
aagctcacc tcactgaggt ctcaggacac gggttgtgca taggaaaggt gccctttacc	2040
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tcagttttta atcagactag agatttctgt atccaggctc agctgattcc tcgcatctat	2220
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cagatcgcca tagatgctga cctccgggcc ctccaagact cagtcagcaa gttagaggac	2460
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tcagggtcag tacgggactc catgaaaaaa ctcaaagaaa aactggataa aagacagtta	2640
gagcgccaga aaagccaaaa ctggtatgaa ggatggttca ataactcccc ttggttcact	2700
acctgtctat caaccatcgc tggggcccta ttactcctcc ttctgttgct catcctcggg	2760
ccatgcatca tcaataagtt agttcaattc atcaatgata ggataagtgc agttaaatt	2820
ctggtcctta gacaaaaata tcaggcccta gagaacgaag gtaaccttta a	2871

<210> 11  
 <211> 956  
 <212> PRT  
 <213> Artificial Sequence



&lt;220&gt;

&lt;223&gt; ScFv-GaLV Env GP chimeric ligand (FvGEL199)

&lt;400&gt; 11

Met Val Leu Leu Pro Gly Ser Met Leu Leu Thr Ser Asn Leu His His  
 1 5 10 15

Leu Arg His Gln Met Ser Pro Gly Ser Trp Lys Arg Leu Ile Ile Leu  
 20 25 30

Leu Ser Cys Val Phe Gly Gly Gly Gly Thr Ser Leu Gln Asn Lys Asn  
 35 40 45

Pro His Gln Pro Met Thr Leu Thr Trp Gln Val Leu Ser Gln Thr Gly  
 50 55 60

Asp Val Val Trp Asp Thr Lys Ala Val Gln Pro Pro Trp Thr Trp Trp  
 65 70 75 80

Pro Thr Leu Lys Pro Asp Val Cys Ala Leu Ala Ala Ser Leu Glu Ser  
 85 90 95

Trp Asp Ile Pro Gly Thr Asp Val Ser Ser Ser Lys Arg Val Arg Pro  
 100 105 110

Pro Asp Ser Asp Tyr Thr Ala Ala Tyr Lys Gln Ile Thr Trp Gly Ala  
 115 120 125

Ile Gly Cys Ser Tyr Pro Arg Ala Arg Thr Arg Met Ala Ser Ser Thr  
 130 135 140

Phe Tyr Val Cys Pro Arg Asp Gly Arg Thr Leu Ser Glu Ala Arg Arg  
 145 150 155 160

Cys Gly Gly Leu Glu Ser Leu Tyr Cys Lys Glu Trp Asp Cys Glu Thr  
 165 170 175

Thr Gly Thr Gly Tyr Trp Leu Ser Lys Ser Ser Lys Asp Leu Ile Thr  
 180 185 190

Val Lys Trp Asp Gln Asn Ser Gly Gly Gly Gly Ser Gln Val Gln Leu  
 195 200 205

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val  
 210 215 220

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp  
 225 230 235 240

Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Phe Ser  
 245 250 255

Pro Gly Asn Asp Asp Phe Lys Tyr Ser Gln Lys Phe Gln Gly Arg Val  
 260 265 270

Thr Ile Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser  
 275 280 285

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu  
 290 295 300

Asp Met Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly  
 305 310 315 320

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile  
 325 330 335

Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg  
 340 345 350

Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn  
 355 360 365

Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro  
 370 375 380

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp  
 385 390 395 400

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
 405 410 415

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr  
 420 425 430

Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ala

435	440	445
Ala Ala Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro Ala		
450	455	460
Ala Gly Gly Gly Gly Ser Glu Trp Thr Gln Lys Phe Gln Gln Cys His		
465	470	475
Gln Thr Gly Trp Cys Asn Pro Leu Lys Ile Asp Phe Thr Asp Lys Gly		
485	490	495
Lys Leu Ser Lys Asp Trp Ile Thr Gly Lys Thr Trp Gly Leu Arg Phe		
500	505	510
Tyr Val Ser Gly His Pro Gly Val Gln Phe Thr Ile Arg Leu Lys Ile		
515	520	525
Thr Asn Met Pro Ala Val Ala Val Gly Pro Asp Leu Val Leu Val Glu		
530	535	540
Gln Gly Pro Pro Arg Thr Ser Leu Ala Leu Pro Pro Pro Leu Pro Pro		
545	550	555
Arg Glu Ala Pro Pro Pro Ser Leu Pro Asp Ser Asn Ser Thr Ala Leu		
565	570	575
Ala Thr Ser Ala Gln Thr Pro Thr Val Arg Lys Thr Ile Val Thr Leu		
580	585	590
Asn Thr Pro Pro Pro Thr Thr Gly Asp Arg Leu Phe Asp Leu Val Gln		
595	600	605
Gly Ala Phe Leu Thr Leu Asn Ala Thr Asn Pro Gly Ala Thr Glu Ser		
610	615	620
Cys Trp Leu Cys Leu Ala Met Gly Pro Pro Tyr Tyr Glu Ala Ile Ala		
625	630	635
Ser Ser Gly Glu Val Ala Tyr Ser Thr Asp Leu Asp Arg Cys Arg Trp		
645	650	655
Gly Thr Gln Gly Lys Leu Thr Leu Thr Glu Val Ser Gly His Gly Leu		
660	665	670

Cys Ile Gly Lys Val Pro Phe Thr His Gln His Leu Cys Asn Gln Thr  
 675 680 685

Leu Ser Ile Asn Ser Ser Gly Asp His Gln Tyr Leu Leu Pro Ser Asn  
 690 695 700

His Ser Trp Trp Ala Cys Ser Thr Gly Leu Thr Pro Cys Leu Ser Thr  
 705 710 715 720

Ser Val Phe Asn Gln Thr Arg Asp Phe Cys Ile Gln Val Gln Leu Ile  
 725 730 735

Pro Arg Ile Tyr Tyr Tyr Pro Glu Glu Val Leu Leu Gln Ala Tyr Asp  
 740 745 750

Asn Ser His Pro Arg Thr Lys Arg Glu Ala Val Ser Leu Thr Leu Ala  
 755 760 765

Val Leu Leu Gly Leu Gly Ile Thr Ala Gly Ile Gly Thr Gly Ser Thr  
 770 775 780

Ala Leu Ile Lys Gly Pro Ile Asp Leu Gln Gln Gly Leu Thr Ser Leu  
 785 790 795 800

Gln Ile Ala Ile Asp Ala Asp Leu Arg Ala Leu Gln Asp Ser Val Ser  
 805 810 815

Lys Leu Glu Asp Ser Leu Thr Ser Leu Ser Glu Val Val Leu Gln Asn  
 820 825 830

Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys Glu Gly Gly Leu Cys Ala  
 835 840 845

Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ile Asp His Ser Gly Ala Val  
 850 855 860

Arg Asp Ser Met Lys Lys Leu Lys Glu Lys Leu Asp Lys Arg Gln Leu  
 865 870 875 880

Glu Arg Gln Lys Ser Gln Asn Trp Tyr Glu Gly Trp Phe Asn Asn Ser  
 885 890 895

Pro Trp Phe Thr Thr Leu Leu Ser Thr Ile Ala Gly Pro Leu Leu Leu  
 900 905 910

Leu Leu Leu Leu Leu Ile Leu Gly Pro Cys Ile Ile Asn Lys Leu Val  
915 920 925

Gln Phe Ile Asn Asp Arg Ile Ser Ala Val Lys Ile Leu Val Leu Arg  
930 935 940

Gln Lys Tyr Gln Ala Leu Glu Asn Glu Gly Asn Leu I  
945 950 955